

Figure 1a / 3**SEQ ID NO:1**

1 MILSLLFSLG GPLGWGLLGA WAQASSTSLS DLQSSRTPGV WKAEAEDTGK DPVGRNWCPY
 61 PMSKLVTLIA LCKTEKFLIH SQQPCPQGAP DCQKVVMYR MAHKPVYQVK QKVLTSIAWR
 121 CCPGYTGPNCE EHHDSMAIPE PADPGDSHQE PQDGPVSFKP GHIAAIVNEV EVQQEQQEHL
 181 LGDLQNDVHR VADSLPGLWK ALPGNLTAAS LSNDVKNVGR CCEAEAGAGA ASLNASLHGL
 241 HNALFATQRS LEQHQRLEFHS LFGNFQGLME ANVSLDLGKL QTMLSRKGKK QOKDLEAPRK
 301 RDKKEAEPLV DIRVTGPVPG ALGAALWEAG SPVAFYASFS EGTAALQTVK FNTTYINIGS
 361 SYFPEHGYFR APERGVYLFA VSVEFGPGPG TGQLVFGGHH RTPVCTTGQG SGSTATVFAM
 421 AELOKGERVW FELTQGSITK RSLSGTAFGG FLMEKT

SEQ ID NO:2

1 ASSTSLSDLQ SSRTPGVWKA EAEDTSKDPV GRNWCPYPMS KLVTLIALCK TEKFLIHSQQ
 61 PCPQGAPDCQ KVKVMYRMAH KPVYQVKQKV LTLAWRCCP GYTGPNCCEH DSMAIPEPAD
 121 PGDSHQEPQD GPVSFKPGHL AAVINEVEVQ QEQQEHLGLD QNDVHRVAD SLPGLWKALP
 181 GNLTAASLSN DVKNVGRCE AEAGAGAASL NASLHGLHNA LFATQRSLEQ HQRLFHSLEFG
 241 NFQGLMEANV SLDLGLQTM LSRKGKKQOK DLEAPRKRDK KEAEPLVDIR VTGPVPGALG
 301 AALWEAGSPV AFYASFSEGT AALQTVKENT TYINIGSSYF PEHGYFRAPE RGVYLFAVSF
 361 EFGPGPGTGQ LVFGGHHRTP VCTTGQSGSGS TATVFAMAELOKGERVWFEL TQGSITKRSL
 421 SGTAFGGFLM FKT

SEQ ID NO:3

1 EAELPLVDIRV TGPVPGALGA ALWEAGSPVA FYASFSEGTALQTVKENTTYINIGSSYFP
 61 EHGFRAPER GYLFVAVSVE FGPVPGTGQL VFGGHRTPV CTTGQSGSGS ATVFAMAELO
 121 KGERVWFELT QGSITKRSLSGTAFGGFLM KT

SEQ ID NO:4

TPVCTTGQGS GSTATVFAMA ELQK

SEQ ID NO:5

VWFELTQGSI TK

SEQ ID NO:6

SLSGTAFGGF LMFK

Figure 1b / 3**SEQ ID NO:7**

1 atgatcctgagcttgctgttcagccttgggggccccctgggctgggggctgctgggggca
61 tgggccaggcttccagtactagcctctctgatctgcagagctccaggacacctggggtc
121 tggaaggcagaggctgaggacaccggcaaggaccccgtaggacgtaactggtgccctac
181 ccaatgtccaagctggtcaccttactagctctttgcaaaacagagaaattcctcatccac
241 tcgcagcagccgtgtccgcagggagctccagactgccagaaagtcaaagtcatgtaccgc
301 atggcccacaagccagtgtaccaggtcaagcagaagggtgctgacctctttggcctggagg
361 tgctgccctggctacacggggcccaactgcgagcaccacgattccatggcaatccctgag
421 cctgcagatcctggtgacagccaccaggaacctcaggatggaccagtcagcttcaaacct
481 ggccaccttgctgcagtgatcaatgaggttgaggtgcaacaggaacagcaggaacatctg
541 ctgggagatctccagaatgatgtgcaccgggtggcagacagcctgccaggcctgtggaaa
601 gccctgcctggtaacctcacagctgcaagcctgagcaacgacgtcaagaatgtcgggcgg
661 tgctgcgaggccgaggccggggccggggccgcctccctcaacgcctcccttcacggcctc
721 cacaacgcactcttcgccactcagcgcagcttggagcagcaccagcggctcttcacagc
781 ctctttgggaacttccaagggtcatggaagccaacgtcagcctggacctggggaagctg
841 cagaccatgctgagcaggaaagggaagaagcagcagaaagacctggaagctccccggaag
901 agggacaagaaggaagcggagcctttggtggacatacgggtcacagggcctgtgccaggt
961 gccttgggcgcggcgctctgggaggcaggatccccctgtggccttctatgccagcttttca
1021 gaaggggacggctgccctgcagacagtgaagttcaacaccacatacatcaacattggcagc
1081 agctacttccctgaacatggctacttccgagccccctgagcgtggtgtctacctgtttgca
1141 gtgagcgttgaaatggccaggggccaggcaccgggcagctggtgtttggaggtcaccat
1201 cggactccagtctgtaccactgggcaggggagtggaagcacagcaacggtctttgccatg
1261 gctgagctgcagaagggtgagcagtatggtttgagtttaaccagggatcaataacaaag
1321 agaagcctgtcgggcactgcatttgggggcttccctgatgtttaagacctga

Figure 2a / 3

10 20 30 40 50 60
ATGATCCTGAGCTTGCTGTTTCAGCCTTGGGGGCCCCCTGGGCTGGGGGCTGCTGGGGGCA
M I L S L L F S L G G P L G W G L L G A

70 80 90 100 110 120
TGGGCCCAGGCTTCCAGTACTAGCCTCTCTGATCTGCAGAGCTCCAGGACACCTGGGGCTC
W A Q A S S T S L S D L Q S S R T P G V

130 140 150 160 170 180
TGGAAGGCAGAGGCTGAGGACACCGGCAAGGACCCCGTAGGACGTAACCTGGTGCCCTAC
W K A E A E D T G K D P V G R N W C P Y

190 200 210 220 230 240
CCAATGTCCAAGCTGGTCACCTTACTAGCTCTTTGCAAAACAGAGAAATTCCTCATCCAC
P M S K L V T L L A L C K T E K F L I H

250 260 270 280 290 300
TCGCAGCAGCCGTGTCCGCAGGGAGCTCCAGACTGCCAGAAAGTCAAAGTCATGTACCGC
S Q Q P C P Q G A P D C Q K V K V M Y R

310 320 330 340 350 360
ATGGCCCACAAGCCAGTGTACCAGGTCAAGCAGAAGGTGCTGACCTCTTTGGCCTGGAGG
M A H K P V Y Q V K Q K V L T S L A W R

370 380 390 400 410 420
TGCTGCCCTGGCTACACGGGCCCCAACTGCGAGCACCACGATTCCATGGCAATCCCTGAG
C C P G Y T G P N C E H H D S M A I P E

430 440 450 460 470 480
CCTGCAGATCCTGGTGACAGCCACCAGGAACCTCAGGATGGACCAGTCAGCTTCAAACCT
P A D P G D S H Q E P Q D G P V S F K P

490 500 510 520 530 540
GGCCACCTTGCTGCAGTGATCAATGAGGTTGAGGTGCAACAGGAACAGCAGGAACATCTG
G H L A A V I N E V E V Q Q E Q Q E H L

550 560 570 580 590 600
CTGGGAGATCTCCAGAATGATGTGCACCGGGTGGCAGACAGCCTGCCAGGCCTGTGGAAA
L G D L Q N D V H R V A D S L P G L W K

610 620 630 640 650 660
GCCCTGCCTGGTAACCTCACAGCTGCAAGCCTGAGCAACGACGTCAAGAATGTCGGGCGG
A L P G N L T A A S L S N D V K N V G R

670 680 690 700 710 720
TGCTGCGAGGCCGAGGCCGGGGCCGGGGCCGCCTCCCTCAACGCCTCCCTTCACGGCCTC
C C E A E A G A G A A S L N A S L H G L

730 740 750 760 770 780
CACAACGCACTCTTCGCCACTCAGCGCAGCTTGGAGCAGCACCAGCGGCTCTTCCACAGC
H N A L F A T Q R S L E Q H Q R L F H S

790 800 810 820 830 840
CTCTTTGGGAACTTCCAAGGGCTCATGGAAGCCAACGTGAGCCTGGACCTGGGGAAAGCTG
L F G N F Q G L M E A N V S L D L G K L

850 860 870 880 890 900
CAGACCATGCTGAGCAGGAAAGGGAAGAAGCAGCAGAAAGACCTGGAAGCTCCCCGGAAG
Q T M L S R K G K K Q Q K D L E A P R K

910 920 930 940 950 960
AGGGACAAGAAGGAAGCGGAGCCTTTGGTGGACATACGGGTACAGGGCCTGTGCCAGGT
R D K K E A E P L V D I R V T G P V P G

Figure 2b / 3

970 980 990 1000 1010 1020
GCCTTGGGCGCGGCTCTGGGAGGCAGGATCCCCTGTGGCCTTCTATGCCAGCTTTTCA
A L G A A L W E A G S P V A F Y A S F S

1030 1040 1050 1060 1070 1080
GAAGGGACGGCTGCCCTGCAGACAGTGAAGTTCAACACCACATACATCAACATTGGCAGC
E G T A A L Q T V K F N T T Y I N I G S

1090 1100 1110 1120 1130 1140
AGCTACTTCCCTGAACATGGCTACTTCCGAGCCCCTGAGCGTGGTGTCTACCTGTTTGCA
S Y F P E H G Y F R A P E R G V Y L F A

1150 1160 1170 1180 1190 1200
GTGAGCGTTGAATTTGGCCCAGGGCCAGGCACCGGGCAGCTGGTGTGTTGGAGGTCACCAT
V S V E F G P G P G T G Q L V F G G H H

1210 1220 1230 1240 1250 1260
CGGACTCCAGTCTGTACCACTGGGCAGGGGAGTGAAGCACAGCAACGGTCTTTGCCATG
R T P V C T T G Q G S G S T A T V F A M

1270 1280 1290 1300 1310 1320
GCTGAGCTGCAGAAGGGTGAGCGAGTATGGTTTGAGTTAACCCAGGGATCAATAACAAAG
A E L Q K G E R V W F E L T Q G S I T K

1330 1340 1350 1360 1370
AGAAGCCTGTTCGGGCACTGCATTTGGGGGCTTCCTGATGTTTAAGACCTGA
R S L S G T A F G G F L M F K T *

Figure 3 / 3

CLUSTAL W (1.81) multiple sequence alignment of SEQ ID NO:1 and Q8K1Z7
(murine homolog)

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SEQ ID NO:1 MILSLLFSLGGPLGWLLGAWAQASSTLSLDLQSSRTPGVWKAEEAEDTGKDPVGRNWCPY
Q8K1Z7      MIPTLLLGFGVYLSWGLLGSWAQDPGTFKFSHLNRPMPGEGWRLGAEDTSRDPIRRNWCPY
          ** :***:.* * .*****:*** ..*.:*.*: . * *: ****.:***: *****

SEQ ID NO:1 PMSKLVTLALCKTEKFLIHSQQPCPQGAPDCQKVVMYRMAHKPVYQVKQKVLTSIAWR
Q8K1Z7      QKSRLVTFVAACKTEKFLVHSQQPCPQGAPDCQGVVMYRVAQKPVYQVQKVLISVDWR
          *:***:.* *****:***** ***** *:***:.*:*****:**** *: **

SEQ ID NO:1 CCPGYTGPNCEHDSMAIPEPADPGDSHQEPQDGPVSFKPGHLAAVINEVEVQQEQQEH
Q8K1Z7      CCPGFQGPDCQDHNPTANPEPTPSGKLQETWDSMDGFELGHPVPEFNEIKVPQEQQE--
          ****: **:*:.*:.* * ****:*... **. *. .*: ** .. :***:.* *****

SEQ ID NO:1 LGDLQNDVHRVADSLPGLWKALPGNLTAASLSNDVKNVGRCCAEAGAGAASLNASLHGL
Q8K1Z7      -----IRRLLSSDVKQIGQCCEASW---AASLNSSLEDL
          **.****:.*:****. *****:***..**

SEQ ID NO:1 HNALFATQRSLEQHQRLFHSFLGNFQGLMEANVSLDLGKLQTMLSRKGGKQKQKLEAPRK
Q8K1Z7      HSMLLDLQHGRLQHRQLFHNLFQNFQGLVASNISLDLGKLQAMLSKKDKKQPRGPGESRK
          *. *: **:*:.*.**:***.* *****: :*:*****:***:*.*** :. .**

SEQ ID NO:1 RDKKEAEPLVDIRVTGPVPGALGAALWEAGSPVAFYASFSEGTAALQTVKFNNTYINIGS
Q8K1Z7      RDKKQVVMSTDAHAKG-----LELWETGSPVAFYAGSSEGATALQMVKNNTTSINVG
          ****:.. *. :..* ****:*****. ***:*** ***** **:**

SEQ ID NO:1 SYFPEHGYFRAPERGVYLFVSVVEFGPGPGTGQLVFEGGHHRTVPVCTTGQSGSTATVFAM
Q8K1Z7      SYFPEHGYFRAPKRGVYLFVSVITFGPGPGMGQLVFEGHHRVPVYSTEQRGGSTATTFAM
          *****:*****: ***** ***** ****.*. * * .*****.***

SEQ ID NO:1 AELQKGERVWFELTQGSITKRSLSGTAFGGFLMFKT
Q8K1Z7      VELQKGERAWFELIQGSATKGSQPGTAFGGFLMFKT
          .*****.***** *** ** * .*****

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